SEQUENCE LISTING

<110> Abrahmsén , Lars
Nilsson, Joakim

<120> METHODS FOR PROTEIN PURIFICATION

<130> 13425-053001

<150> SE 0100625-3
<151> 2001-02-23

<150> US 60/272,247
<151> 2001-02-28

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4040
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (161)...(2449)

<400> 1

```
gtccttccca cccttagtcc caggcatctg actaccggga acctcagcca gagtccggga     60
gccccccacc ccgtccagga gccaacagag cccccgtctt gctggcgtga gaatacattg    120
ctctcctttg gttgaatcag ctgtccctct tcgtgggaaa atg aac cag aag aca      175
                                              Met Asn Gln Lys Thr
                                               1               5

atc ctc gtg ctc ctc att ctg gcc gtc atc acc atc ttt gcc ttg gtt      223
Ile Leu Val Leu Leu Ile Leu Ala Val Ile Thr Ile Phe Ala Leu Val
                 10                  15                  20

tgt gtc ctg ctg gtg ggc agg ggt gga gat ggg ggt gaa ccc agc cag      271
Cys Val Leu Leu Val Gly Arg Gly Gly Asp Gly Gly Glu Pro Ser Gln
             25                  30                  35

ctt ccc cat tgc ccc tct gta tct ccc agt gcc cag cct tgg aca cac      319
Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala Gln Pro Trp Thr His
         40                  45                  50

cct ggc cag agc cag ctg ttt gca gac ctg agc cga gag gag ctg acg      367
Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser Arg Glu Glu Leu Thr
     55                  60                  65

gct gtg atg cgc ttt ctg acc cag cgg ctg ggg cca ggg ctg gtg gat      415
Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly Pro Gly Leu Val Asp
 70                  75                  80                  85
```

```
gca gcc cag gcc cgg ccc tcg gac aac tgt gtc ttc tca gtg gag ttg      463
Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val Phe Ser Val Glu Leu
                 90                  95                 100

cag ctg cct ccc aag gct gca gcc ctg gct cac ttg gac agg ggg agc      511
Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His Leu Asp Arg Gly Ser
            105                 110                 115

ccc cca cct gcc cgg gag gca ctg gcc atc gtc ttc ttt ggc agg caa      559
Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val Phe Phe Gly Arg Gln
        120                 125                 130

ccc cag ccc aac gtg agt gag ctg gtg gtg ggg cca ctg cct cac ccc      607
Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly Pro Leu Pro His Pro
    135                 140                 145

tcc tac atg cgg gac gtg act gtg gag cgt cat gga ggc ccc ctg ccc      655
Ser Tyr Met Arg Asp Val Thr Val Glu Arg His Gly Gly Pro Leu Pro
150                 155                 160                 165

tat cac cga cgc ccc gtg ctg ttc caa gag tac ctg gac ata gac cag      703
Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr Leu Asp Ile Asp Gln
                170                 175                 180

atg atc ttc aac aga gag ctg ccc cag gct tct ggg ctt ctc cac cac      751
Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser Gly Leu Leu His His
            185                 190                 195

tgt tgc ttc tac aag cac cgg gga cgg aac ctg gtg aca atg acc acg      799
Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu Val Thr Met Thr Thr
        200                 205                 210

gct ccc cgt ggt ctg caa tca ggg gac cgg gcc acc tgg ttt ggc ctc      847
Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala Thr Trp Phe Gly Leu
    215                 220                 225

tac tac aac atc tcg ggc gct ggg ttc ttc ctg cac cac gtg ggc ttg      895
Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu His His Val Gly Leu
230                 235                 240                 245

gag ctg cta gtg aac cac aag gcc ctt gac cct gcc cgc tgg act atc      943
Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro Ala Arg Trp Thr Ile
                250                 255                 260

cag aag gtg ttc tat caa ggc cgc tac tac gac agc ctg gcc cag ctg      991
Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp Ser Leu Ala Gln Leu
            265                 270                 275

gag gcc cag ttt gag gcc ggc ctg gtg aat gtg gtg ctg atc cca gac     1039
Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val Val Leu Ile Pro Asp
        280                 285                 290

aat ggc aca ggt ggg tcc tgg tcc ctg aag tcc cct gtg ccc ccg ggt     1087
Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser Pro Val Pro Pro Gly
    295                 300                 305

cca gct ccc cct cta cag ttc tat ccc caa ggc ccc cgc ttc agt gtc     1135
```

```
Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly Pro Arg Phe Ser Val
310                 315                 320                 325

cag gga agt cga gtg gcc tcc tca ctg tgg act ttc tcc ttt ggc ctc     1183
Gln Gly Ser Arg Val Ala Ser Ser Leu Trp Thr Phe Ser Phe Gly Leu
                330                 335                 340

gga gca ttc agt ggc cca agg atc ttt gac gtt cgc ttc caa gga gaa     1231
Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val Arg Phe Gln Gly Glu
            345                 350                 355

aga cta gtt tat gag ata agc ctc caa gag gcc ttg gcc atc tat ggt     1279
Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala Leu Ala Ile Tyr Gly
        360                 365                 370

gga aat tcc cca gca gca atg acg acc cgc tat gtg gat gga ggc ttt     1327
Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr Val Asp Gly Gly Phe
    375                 380                 385

ggc atg ggc aag tac acc acg ccc ctg acc cgt ggg gtg gac tgc ccc     1375
Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg Gly Val Asp Cys Pro
390                 395                 400                 405

tac ttg gcc acc tac gtg gac tgg cac ttc ctt ttg gag tcc cag gcc     1423
Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu Leu Glu Ser Gln Ala
                410                 415                 420

ccc aag aca ata cgt gat gcc ttt tgt gtg ttt gaa cag aac cag ggc     1471
Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe Glu Gln Asn Gln Gly
            425                 430                 435

ctc ccc ctg cgg cga cac cac tca gat ctc tac tcg cac tac ttt ggg     1519
Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly
        440                 445                 450

ggt ctt gcg gaa acg gtg ctg gtc gtc aga tct atg tcc acc ttg ctc     1567
Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser Met Ser Thr Leu Leu
    455                 460                 465

aac tat gac tat gtg tgg gat acg gtc ttc cac ccc agt ggg gcc ata     1615
Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile
470                 475                 480                 485

gaa ata cga ttc tat gcc acg ggc tac atc agc tcg gca ttc ctc ttt     1663
Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe
                490                 495                 500

ggt gct act ggg aag tac ggg aac caa gtg tca gag cac acc ctg ggc     1711
Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly
            505                 510                 515

acg gtc cac acc cac agc gcc cac ttc aag gtg gat ctg gat gta gca     1759
Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala
        520                 525                 530

gga ctg gag aac tgg gtc tgg gcc gag gat atg gtc ttt gtc ccc atg     1807
Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met
```

```
    535                 540                 545

gct gtg ccc tgg agc cct gag cac cag ctg cag agg ctg cag gtg acc     1855
Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr
550                 555                 560                 565

cgg aag ctg ctg gag atg gag gag cag gcc gcc ttc ctc gtg gga agc     1903
Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser
                570                 575                 580

gcc acc cct cgc tac ctg tac ctg gcc agc aac cac agc aac aag tgg     1951
Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp
            585                 590                 595

ggt cac ccc cgg ggc tac cgc atc cag atg ctc agc ttt gct gga gag     1999
Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu
        600                 605                 610

ccg ctg ccc caa aac agc tcc atg gcg aga ggc ttc agc tgg gag agg     2047
Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg
    615                 620                 625

tac cag ctg gct gtg acc cag cgg aag gag gag gag ccc agt agc agc     2095
Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser
630                 635                 640                 645

agc gtt ttc aat cag aat gac cct tgg gcc ccc act gtg gat ttc agt     2143
Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro Thr Val Asp Phe Ser
                650                 655                 660

gac ttc atc aac aat gag acc att gct gga aag gat ttg gtg gcc tgg     2191
Asp Phe Ile Asn Asn Glu Thr Ile Ala Gly Lys Asp Leu Val Ala Trp
            665                 670                 675

gtg aca gct ggt ttt ctg cat atc cca cat gca gag gac att cct aac     2239
Val Thr Ala Gly Phe Leu His Ile Pro His Ala Glu Asp Ile Pro Asn
        680                 685                 690

aca gtg act gtg ggg aac ggc gtg ggc ttc ttc ctc cga ccc tat aac     2287
Thr Val Thr Val Gly Asn Gly Val Gly Phe Phe Leu Arg Pro Tyr Asn
    695                 700                 705

ttc ttt gac gaa gac ccc tcc ttc tac tct gcc gac tcc atc tac ttc     2335
Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala Asp Ser Ile Tyr Phe
710                 715                 720                 725

cga ggg gac cag gat gct ggg gcc tgc gag gtc aac ccc cta gct tgc     2383
Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val Asn Pro Leu Ala Cys
                730                 735                 740

ctg ccc cag gct gct gcc tgt gcc ccc gac ctc cct gcc ttc tcc cac     2431
Leu Pro Gln Ala Ala Ala Cys Ala Pro Asp Leu Pro Ala Phe Ser His
            745                 750                 755

ggg ggc ttc tct cac aac taggcggtcc tgggatgggg catgtggcca            2479
Gly Gly Phe Ser His Asn
        760
```

```
agggctccag ggccagggtg tgagggatgg ggagcagctg ggcactgggc cggcagcctg   2539
gttccctctt tcctgtgcca ggactctctt tcttccacta ccctccctcg catccgcctc   2599
tgagccagga gcctcctgac cctgtgatgc ctgacacagg ggacactgaa ccttgttgat   2659
gccagctgta ctgagttctc atccacagag gccaggcatg gcccagcctg gagccgtggc   2719
cgagggcttc cctagatggt tccctttgtt gctgtctggc tttcccgaat ctttttaggc   2779
cacctccaag gactctaaaa gggggctatt ccctggagac cccagagtag ggttgccagt   2839
cctgcaagtc catagctgag ctggaaagga tgcttctgct cacattccct ctcatccagg   2899
tcctttcctt ctcgtcttcc tctctctcac ctacttcctc ctcctcctcc tgttcctgcc   2959
ttctcttcta tcctgcaatt tctcccgaat cctgagggga tatccctatg tcccagcccc   3019
tggtactccc ccagccctca gttttcagtc aagttccgtc tcctctccag ccctatggaa   3079
gtctcaaggt cacgggaccc ctaatcagag tggccaatcc ctgtgtgtcg ttcccttgtg   3139
tctgttgctt attgggagta ggagttgctc ctacccctgt cctggggctg ggtgtgtttc   3199
aggacagctg cttctgtgca tttgtgtctg cctgcctcat gctctctata gaggaggatg   3259
gtcatcgtga cagcagcagc tcaagttagc atttcaagtg atttgggggt gcaatgataa   3319
tgaagaatgg ccattttgta ccagggctct gtattctgca acagcctgtt tgggaggctg   3379
gagtggaaac aaagggtggg catcaaagat gagaagccaa agcccctaca actccagcca   3439
cccagccagg aggggctgtc caatcacatt caggcatgcg aatgagctgg gccctgggtg   3499
aggtgggggt ctggcctagt ggggaggggc ctggcctggg tggggcaggg cctggcctgg   3559
tccaggcttg ggctccattc ccatcactgc tgtccctcct gaggtctgga ttggggatgg   3619
ggacaaagaa atagcaagag atgagaaaca acagaaactt ttttctctaa aggactggtt   3679
aaatcaattc tgatacagcc ttacaataca atagtatgca gctaaaaaat aattgtatgt   3739
ctttatatac taatatgtaa taatcttcag gtgaaaaagg caagccacag aaatgtgtat   3799
agcgcacttc ccatttgtgt ttcagaaagg agtagaatat aaacacataa ttgcttatgt   3859
atgcctattc agaataaatg ggtaacactg attacttttg ggaggggaac cagtaggttg   3919
aggacaggag agggaagggt cttaacactt acacccttttt gtacattttg aattttgaac   3979
catgtgactg tattacctat tcaaaataaa caataaatgg gcccaaaaaa aaaaaaaaaa   4039
a                                                                   4040
```

<210> 2
<211> 763
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Asn Gln Lys Thr Ile Leu Val Leu Leu Ile Leu Ala Val Ile Thr
 1               5                  10                  15
Ile Phe Ala Leu Val Cys Val Leu Leu Val Gly Arg Gly Gly Asp Gly
            20                  25                  30
Gly Glu Pro Ser Gln Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala
        35                  40                  45
Gln Pro Trp Thr His Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser
    50                  55                  60
Arg Glu Glu Leu Thr Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly
65                  70                  75                  80
Pro Gly Leu Val Asp Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val
                85                  90                  95
Phe Ser Val Glu Leu Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His
            100                 105                 110
Leu Asp Arg Gly Ser Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val
        115                 120                 125
Phe Phe Gly Arg Gln Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly
    130                 135                 140
Pro Leu Pro His Pro Ser Tyr Met Arg Asp Val Thr Val Glu Arg His
145                 150                 155                 160
Gly Gly Pro Leu Pro Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr
                165                 170                 175
```

```
Leu Asp Ile Asp Gln Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser
            180                 185                 190
Gly Leu Leu His His Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu
        195                 200                 205
Val Thr Met Thr Thr Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala
    210                 215                 220
Thr Trp Phe Gly Leu Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu
225                 230                 235                 240
His His Val Gly Leu Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro
                245                 250                 255
Ala Arg Trp Thr Ile Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp
            260                 265                 270
Ser Leu Ala Gln Leu Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val
        275                 280                 285
Val Leu Ile Pro Asp Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser
    290                 295                 300
Pro Val Pro Pro Gly Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly
305                 310                 315                 320
Pro Arg Phe Ser Val Gln Gly Ser Arg Val Ala Ser Ser Leu Trp Thr
                325                 330                 335
Phe Ser Phe Gly Leu Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val
            340                 345                 350
Arg Phe Gln Gly Glu Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala
        355                 360                 365
Leu Ala Ile Tyr Gly Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr
    370                 375                 380
Val Asp Gly Gly Phe Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg
385                 390                 395                 400
Gly Val Asp Cys Pro Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu
                405                 410                 415
Leu Glu Ser Gln Ala Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe
            420                 425                 430
Glu Gln Asn Gln Gly Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr
        435                 440                 445
Ser His Tyr Phe Gly Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser
    450                 455                 460
Met Ser Thr Leu Leu Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His
465                 470                 475                 480
Pro Ser Gly Ala Ile Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser
                485                 490                 495
Ser Ala Phe Leu Phe Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser
            500                 505                 510
Glu His Thr Leu Gly Thr Val His Thr His Ser Ala His Phe Lys Val
        515                 520                 525
Asp Leu Asp Val Ala Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met
    530                 535                 540
Val Phe Val Pro Met Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln
545                 550                 555                 560
Arg Leu Gln Val Thr Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala
                565                 570                 575
Phe Leu Val Gly Ser Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn
            580                 585                 590
His Ser Asn Lys Trp Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu
        595                 600                 605
Ser Phe Ala Gly Glu Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly
    610                 615                 620
Phe Ser Trp Glu Arg Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu
```

```
625                 630                 635                 640
Glu Pro Ser Ser Ser Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro
                645                 650                 655
Thr Val Asp Phe Ser Asp Phe Ile Asn Asn Glu Thr Ile Ala Gly Lys
            660                 665                 670
Asp Leu Val Ala Trp Val Thr Ala Gly Phe Leu His Ile Pro His Ala
        675                 680                 685
Glu Asp Ile Pro Asn Thr Val Thr Val Gly Asn Gly Val Gly Phe Phe
    690                 695                 700
Leu Arg Pro Tyr Asn Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala
705                 710                 715                 720
Asp Ser Ile Tyr Phe Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val
                725                 730                 735
Asn Pro Leu Ala Cys Leu Pro Gln Ala Ala Ala Cys Ala Pro Asp Leu
            740                 745                 750
Pro Ala Phe Ser His Gly Gly Phe Ser His Asn
        755                 760
```

<210> 3
<211> 739
<212> DNA
<213> Schistosoma japonicum

<220>
<221> CDS
<222> (17)...(670)

<400> 3

```
tttaggtaac ttggtc atg tcc cct ata cta ggt tat tgg aaa att aag ggc      52
                   Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly
                    1               5                   10

ctt gtg caa ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat      100
Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr
          15                  20                  25

gaa gag cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa      148
Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys
      30                  35                  40

aag ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat      196
Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
  45                  50                  55                  60

ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata gct      244
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala
                  65                  70                  75

gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca gag att      292
Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile
              80                  85                  90

tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt gtt tcg aga      340
Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg
          95                  100                 105

att gca tat agt aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc      388
```

```
Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser
    110                 115                 120

aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa      436
Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys
125                 130                 135                 140

aca tat tta aat ggt gat cat gta acc cat cct gac ttc atg ttg tat      484
Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr
                145                 150                 155

gac gct ctt gat gtt gtt tta tac atg gac cca atg tgc ctg gat gcg      532
Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala
            160                 165                 170

ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa      580
Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln
        175                 180                 185

att gat aag tac ttg aaa tcc agc aag tat ata gca tgg cct ttg cag      628
Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln
    190                 195                 200

ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct cca aaa              670
Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys
205                 210                 215

taaattaaga atgattgttt tagtaaacat tatttatcac ttacaattaa actaaatata    730
aatgtcgac                                                            739

<210> 4
<211> 218
<212> PRT
<213> Schistosoma japonicum

<400> 4
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1               5                  10                  15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
```

```
                165                 170                 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys
    210                 215

<210> 5
<211> 218
<212> PRT
<213> Schistosoma japonicum

<400> 5
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1               5                  10                  15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80
Met Leu Gly Gly Ser Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125
Met Leu Lys Met Phe Glu Asp Arg Leu Ser His Lys Thr Tyr Leu Asn
    130                 135                 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175
Val Ser Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys
    210                 215

<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Protease cleavage site

<400> 6
Glu Ala Leu Phe Gln Gly
 1               5

<210> 7
<211> 43
```

<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 7
ccggaattcc aacgcgtcca tgaaccagaa gacaatcctc gtg 43

<210> 8
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 8
cccccaagct tgtcgactca ctagttgtga gagagaagcc ccccc 45

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 9
gaggaagctt tgttccaagg tggagatggg ggtgaa 36

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 10
gcattctagt tgtggtttgt c 21

<210> 11
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 11
gccggaattc gacgcgtccc ctatactagg ttattgg 37

<210> 12
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 12
ctctgcgcgc tcttttggag aacccaacat gttgtgc 37

<210> 13
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 13
ggttctccaa aagagcgcgc agagatttca atgcttgaag 40

<210> 14
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 14
atgagataaa cggtcttcga acattttcag catttc 36

<210> 15
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 15
gttcgaagac cgtttatctc ataaaacata tttaaatggt gatc 44

<210> 16
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 16
aaaagaaact agttttggga acgcatccag gca 33

<210> 17
<211> 40
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer

<400> 17
cccaaaacta gtttctttta aaaaacgtat tgaagctatc 40

<210> 18
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 18
acccaagctt cctgactttg tgactttgga ggatggtcgc cacc 44

<210> 19
<211> 3006
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant construct

<221> CDS
<222> (1)...(2994)

<400> 19
atg gat tgg ctg cgg aac ttg cta ttc ctg atg gcg gcc gct caa agt 48
Met Asp Trp Leu Arg Asn Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15

atc aac gcc gcg caa cac gat gaa gcc gta gac aac aaa ttc aac aaa 96
Ile Asn Ala Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
20 25 30

gaa caa caa aac gcg tcc cct ata cta ggt tat tgg aaa att aag ggc 144
Glu Gln Gln Asn Ala Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly
35 40 45

ctt gtg caa ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat 192
Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr
50 55 60

gaa gag cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa 240
Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys
65 70 75 80

aag ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat 288
Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
85 90 95

ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata gct 336
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala
100 105 110

gac aag cac aac atg ttg ggt ggt tct cca aaa gag cgc gca gag att 384

```
Asp Lys His Asn Met Leu Gly Gly Ser Pro Lys Glu Arg Ala Glu Ile
        115                 120                 125

tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt gtt tcg aga      432
Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg
    130                 135                 140

att gca tat agt aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc      480
Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser
145                 150                 155                 160

aag cta cct gaa atg ctg aaa atg ttc gaa gac cgt tta tct cat aaa      528
Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Ser His Lys
                165                 170                 175

aca tat tta aat ggt gat cat gta acc cat cct gac ttc atg ttg tat      576
Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr
            180                 185                 190

gac gct ctt gat gtt gtt tta tac atg gac cca atg tgc ctg gat gcg      624
Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala
        195                 200                 205

ttc cca aaa cta gtt tct ttt aaa aaa cgt att gaa gct atc cca caa      672
Phe Pro Lys Leu Val Ser Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln
    210                 215                 220

att gat aag tac ttg aaa tcc agc aag tat ata gca tgg cct ttg cag      720
Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln
225                 230                 235                 240

ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct cca aag tca caa      768
Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Gln
                245                 250                 255

agt cag gaa gct ttg ttc caa ggt gga gat ggg ggt gaa ccc agc cag      816
Ser Gln Glu Ala Leu Phe Gln Gly Gly Asp Gly Gly Glu Pro Ser Gln
            260                 265                 270

ctt ccc cat tgc ccc tct gta tct ccc agt gcc cag cct tgg aca cac      864
Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala Gln Pro Trp Thr His
        275                 280                 285

cct ggc cag agc cag ctg ttt gca gac ctg agc cga gag gag ctg acg      912
Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser Arg Glu Glu Leu Thr
    290                 295                 300

gct gtg atg cgc ttt ctg acc cag cgg ctg ggg cca ggg ctg gtg gat      960
Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly Pro Gly Leu Val Asp
305                 310                 315                 320

gca gcc cag gcc cgg ccc tcg gac aac tgt gtc ttc tca gtg gag ttg     1008
Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val Phe Ser Val Glu Leu
                325                 330                 335

cag ctg cct ccc aag gct gca gcc ctg gct cac ttg gac agg ggg agc     1056
Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His Leu Asp Arg Gly Ser
```

340 345 350

ccc cca cct gcc cgg gag gca ctg gcc atc gtc ttc ttt ggc agg caa 1104
Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val Phe Phe Gly Arg Gln
355 360 365

ccc cag ccc aac gtg agt gag ctg gtg gtg ggg cca ctg cct cac ccc 1152
Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly Pro Leu Pro His Pro
370 375 380

tcc tac atg cgg gac gtg act gtg gag cgt cat gga ggc ccc ctg ccc 1200
Ser Tyr Met Arg Asp Val Thr Val Glu Arg His Gly Gly Pro Leu Pro
385 390 395 400

tat cac cga cgc ccc gtg ctg ttc caa gag tac ctg gac ata gac cag 1248
Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr Leu Asp Ile Asp Gln
405 410 415

atg atc ttc aac aga gag ctg ccc cag gct tct ggg ctt ctc cac cac 1296
Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser Gly Leu Leu His His
420 425 430

tgt tgc ttc tac aag cac cgg gga cgg aac ctg gtg aca atg acc acg 1344
Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu Val Thr Met Thr Thr
435 440 445

gct ccc cgt ggt ctg caa tca ggg gac cgg gcc acc tgg ttt ggc ctc 1392
Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala Thr Trp Phe Gly Leu
450 455 460

tac tac aac atc tcg ggc gct ggg ttc ttc ctg cac cac gtg ggc ttg 1440
Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu His His Val Gly Leu
465 470 475 480

gag ctg cta gtg aac cac aag gcc ctt gac cct gcc cgc tgg act atc 1488
Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro Ala Arg Trp Thr Ile
485 490 495

cag aag gtg ttc tat caa ggc cgc tac tac gac agc ctg gcc cag ctg 1536
Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp Ser Leu Ala Gln Leu
500 505 510

gag gcc cag ttt gag gcc ggc ctg gtg aat gtg gtg ctg atc cca gac 1584
Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val Val Leu Ile Pro Asp
515 520 525

aat ggc aca ggt ggg tcc tgg tcc ctg aag tcc cct gtg ccc ccg ggt 1632
Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser Pro Val Pro Pro Gly
530 535 540

cca gct ccc cct cta cag ttc tat ccc caa ggc ccc cgc ttc agt gtc 1680
Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly Pro Arg Phe Ser Val
545 550 555 560

cag gga agt cga gtg gcc tcc tca ctg tgg act ttc tcc ttt ggc ctc 1728
Gln Gly Ser Arg Val Ala Ser Ser Leu Trp Thr Phe Ser Phe Gly Leu
565 570 575

gga gca ttc agt ggc cca agg atc ttt gac gtt cgc ttc caa gga gaa 1776
Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val Arg Phe Gln Gly Glu
580 585 590

aga cta gtt tat gag ata agc ctc caa gag gcc ttg gcc atc tat ggt 1824
Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala Leu Ala Ile Tyr Gly
595 600 605

gga aat tcc cca gca gca atg acg acc cgc tat gtg gat gga ggc ttt 1872
Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr Val Asp Gly Gly Phe
610 615 620

ggc atg ggc aag tac acc acg ccc ctg acc cgt ggg gtg gac tgc ccc 1920
Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg Gly Val Asp Cys Pro
625 630 635 640

tac ttg gcc acc tac gtg gac tgg cac ttc ctt ttg gag tcc cag gcc 1968
Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu Leu Glu Ser Gln Ala
645 650 655

ccc aag aca ata cgt gat gcc ttt tgt gtg ttt gaa cag aac cag ggc 2016
Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe Glu Gln Asn Gln Gly
660 665 670

ctc ccc ctg cgg cga cac cac tca gat ctc tac tcg cac tac ttt ggg 2064
Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly
675 680 685

ggt ctt gcg gaa acg gtg ctg gtc gtc aga tct atg tcc acc ttg ctc 2112
Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser Met Ser Thr Leu Leu
690 695 700

aac tat gac tat gtg tgg gat acg gtc ttc cac ccc agt ggg gcc ata 2160
Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile
705 710 715 720

gaa ata cga ttc tat gcc acg ggc tac atc agc tcg gca ttc ctc ttt 2208
Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe
725 730 735

ggt gct act ggg aag tac ggg aac caa gtg tca gag cac acc ctg ggc 2256
Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly
740 745 750

acg gtc cac acc cac agc gcc cac ttc aag gtg gat ctg gat gta gca 2304
Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala
755 760 765

gga ctg gag aac tgg gtc tgg gcc gag gat atg gtc ttt gtc ccc atg 2352
Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met
770 775 780

gct gtg ccc tgg agc cct gag cac cag ctg cag agg ctg cag gtg acc 2400
Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr
785 790 795 800

```
cgg aag ctg ctg gag atg gag gag cag gcc gcc ttc ctc gtg gga agc     2448
Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser
                805                 810                 815

gcc acc cct cgc tac ctg tac ctg gcc agc aac cac agc aac aag tgg     2496
Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp
            820                 825                 830

ggt cac ccc cgg ggc tac cgc atc cag atg ctc agc ttt gct gga gag     2544
Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu
        835                 840                 845

ccg ctg ccc caa aac agc tcc atg gcg aga ggc ttc agc tgg gag agg     2592
Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg
    850                 855                 860

tac cag ctg gct gtg acc cag cgg aag gag gag gag ccc agt agc agc     2640
Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser
865                 870                 875                 880

agc gtt ttc aat cag aat gac cct tgg gcc ccc act gtg gat ttc agt     2688
Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro Thr Val Asp Phe Ser
                885                 890                 895

gac ttc atc aac aat gag acc att gct gga aag gat ttg gtg gcc tgg     2736
Asp Phe Ile Asn Asn Glu Thr Ile Ala Gly Lys Asp Leu Val Ala Trp
            900                 905                 910

gtg aca gct ggt ttt ctg cat atc cca cat gca gag gac att cct aac     2784
Val Thr Ala Gly Phe Leu His Ile Pro His Ala Glu Asp Ile Pro Asn
        915                 920                 925

aca gtg act gtg ggg aac ggc gtg ggc ttc ttc ctc cga ccc tat aac     2832
Thr Val Thr Val Gly Asn Gly Val Gly Phe Phe Leu Arg Pro Tyr Asn
    930                 935                 940

ttc ttt gac gaa gac ccc tcc ttc tac tct gcc gac tcc atc tac ttc     2880
Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala Asp Ser Ile Tyr Phe
945                 950                 955                 960

cga ggg gac cag gat gct ggg gcc tgc gag gtc aac ccc cta gct tgc     2928
Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val Asn Pro Leu Ala Cys
                965                 970                 975

ctg ccc cag gct gct gcc tgt gcc ccc gac ctc cct gcc ttc tcc cac     2976
Leu Pro Gln Ala Ala Ala Cys Ala Pro Asp Leu Pro Ala Phe Ser His
            980                 985                 990

ggg ggc ttc tct cac aac tagtgagtcg ac                               3006
Gly Gly Phe Ser His Asn
        995
```

<210> 20
<211> 998
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombinant construct

<400> 20

```
Met Asp Trp Leu Arg Asn Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
 1               5                  10                  15
Ile Asn Ala Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
            20                  25                  30
Glu Gln Gln Asn Ala Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly
        35                  40                  45
Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr
    50                  55                  60
Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys
65                  70                  75                  80
Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
                85                  90                  95
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala
            100                 105                 110
Asp Lys His Asn Met Leu Gly Gly Ser Pro Lys Glu Arg Ala Glu Ile
        115                 120                 125
Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg
    130                 135                 140
Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser
145                 150                 155                 160
Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Ser His Lys
                165                 170                 175
Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr
            180                 185                 190
Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala
        195                 200                 205
Phe Pro Lys Leu Val Ser Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln
    210                 215                 220
Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln
225                 230                 235                 240
Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Gln
                245                 250                 255
Ser Gln Glu Ala Leu Phe Gln Gly Gly Asp Gly Gly Glu Pro Ser Gln
            260                 265                 270
Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala Gln Pro Trp Thr His
        275                 280                 285
Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser Arg Glu Glu Leu Thr
    290                 295                 300
Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly Pro Gly Leu Val Asp
305                 310                 315                 320
Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val Phe Ser Val Glu Leu
                325                 330                 335
Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His Leu Asp Arg Gly Ser
            340                 345                 350
Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val Phe Phe Gly Arg Gln
        355                 360                 365
Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly Pro Leu Pro His Pro
    370                 375                 380
Ser Tyr Met Arg Asp Val Thr Val Glu Arg His Gly Gly Pro Leu Pro
385                 390                 395                 400
Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr Leu Asp Ile Asp Gln
                405                 410                 415
```

```
Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser Gly Leu Leu His His
            420                 425                 430
Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu Val Thr Met Thr Thr
        435                 440                 445
Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala Thr Trp Phe Gly Leu
    450                 455                 460
Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu His His Val Gly Leu
465                 470                 475                 480
Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro Ala Arg Trp Thr Ile
                485                 490                 495
Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp Ser Leu Ala Gln Leu
            500                 505                 510
Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val Val Leu Ile Pro Asp
        515                 520                 525
Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser Pro Val Pro Pro Gly
    530                 535                 540
Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly Pro Arg Phe Ser Val
545                 550                 555                 560
Gln Gly Ser Arg Val Ala Ser Ser Leu Trp Thr Phe Ser Phe Gly Leu
                565                 570                 575
Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val Arg Phe Gln Gly Glu
            580                 585                 590
Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala Leu Ala Ile Tyr Gly
        595                 600                 605
Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr Val Asp Gly Gly Phe
    610                 615                 620
Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg Gly Val Asp Cys Pro
625                 630                 635                 640
Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu Leu Glu Ser Gln Ala
                645                 650                 655
Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe Glu Gln Asn Gln Gly
            660                 665                 670
Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly
        675                 680                 685
Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser Met Ser Thr Leu Leu
    690                 695                 700
Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile
705                 710                 715                 720
Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe
                725                 730                 735
Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly
            740                 745                 750
Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala
        755                 760                 765
Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met
    770                 775                 780
Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr
785                 790                 795                 800
Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser
                805                 810                 815
Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp
            820                 825                 830
Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu
        835                 840                 845
Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg
    850                 855                 860
Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser
```

```
865                     870                     875                     880
Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro Thr Val Asp Phe Ser
                885                     890                     895
Asp Phe Ile Asn Asn Glu Thr Ile Ala Gly Lys Asp Leu Val Ala Trp
            900                     905                     910
Val Thr Ala Gly Phe Leu His Ile Pro His Ala Glu Asp Ile Pro Asn
        915                     920                     925
Thr Val Thr Val Gly Asn Gly Val Gly Phe Phe Leu Arg Pro Tyr Asn
    930                     935                     940
Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala Asp Ser Ile Tyr Phe
945                     950                     955                     960
Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val Asn Pro Leu Ala Cys
                965                     970                     975
Leu Pro Gln Ala Ala Ala Cys Ala Pro Asp Leu Pro Ala Phe Ser His
            980                     985                     990
Gly Gly Phe Ser His Asn
        995
```